Appendix

A.1 Choice of Prior Distributions

We define the prior distributions of the α's as (improper) uniform distributions, Normal(0,10000) priors for the $\boldsymbol{\beta}_j$'s, and the prior distributions of the $\mathbf{U}$ as multiCAR. For the general case, the multiCAR prior on $\mathbf{U}$ is defined in terms of county i's multivariate p-dimensional vector of spatially correlated Normal random effects, $\mathbf{U}_i = (U_{1i}, U_{2i}, \ldots, U_{pi})'$, so that $\mathbf{U} = (\mathbf{U}_1, \mathbf{U}_2, \ldots, \mathbf{U}_i)$. In the present research we compare two racial groups, so $p = 2$; we define the prior distribution on $\mathbf{U_i}$ as

$$\mathbf{U}_i | \mathbf{U}_{(-i)} \backsim N_2(\overline{\mathbf{U}}_i, \frac{\mathbf{\Lambda}}{m_i}) \ , \tag{1}$$

where $\overline{\mathbf{U}}_i = (\overline{U}_{1i}, \overline{U}_{2i})'$ has $\overline{U}_{qi} = \sum_{j \in \kappa_i} \frac{U_{qj}}{m_i}$, with κ_i the set of "neighbors" of county i (typically and here defined by adjacency) and with $m_i = |\kappa_i|$ the number of neighbors of county i, where $i \notin \kappa_i$ by convention, and where $\mathbf{U}_{(-i)}$ is the 2 by $(I-1)$ sub-matrix of $\mathbf{U}$ with the i^{th} column deleted. By specifying the prior distributions on the $\mathbf{U}$ as multiCAR, we allow for intra-county correlation between rate estimates for the two racial groups in a given county. The relative variability and covariance relationships between stroke death rates for the two racial groups is described by $\mathbf{\Lambda}$. For county i, $\frac{\mathbf{\Lambda}}{m_i}$ incorporates the number of neighbors of the county into the conditional covariance matrix. To complete the model, we specify hyperparameters for the prior distribution of the variance matrix. We assign a conjugate inverse Wishart prior distribution to $\mathbf{\Lambda}$. Although our model definition includes improper prior distributions for the α's and the $\mathbf{U}$, the propriety of the resulting posterior distributions have been addressed by Ghosh et al.[1] and Sun et al.[2]

A.2 Implementation

We implemented our fully Bayesian model using Markov chain Monte Carlo (MCMC) methods. Such iterative MCMC methods, detailed in Gilks et al.,[3] allow generation of post-convergence samples from the (approximate) posterior distribution of parameters of interest and overcome potentially intractable integration in our models. From these samples, we calculate and map standard properties, such as the median and 95 percent credible intervals and other quantities of interest. We used WinBugs 1.4.1 to execute our model, created maps with ArcView 3.3 (ESRI, Redlands, CA), and produced graphs and performed many calculations with R-2.1.1 (R Foundation for Statistical Computing, Vienna, Austria).

In all implementations we ran three overdispersed, random, parallel chains of 15,000 MCMC simulations each, discarding the first 5,000 samples from each chain as a burn-in period for a total of 30,000 simulations. Convergence was adequate on the basis of both formal Gelman and Rubin diagnostics and informal visual inspection of the mixing of the multiple chains.[4] For all models, we estimated quantities of interest (such as racial disparity and race-specific stroke death rates) as the median value from the MCMC iterations, which represent approximate samples from the posterior distribution of the quantity conditional on the data.

References

[1] Ghosh M, Natarajan K, Waller LA, Kim D. Hierarchical Bayes GLMs for the analysis of spatial data: an application to disease mapping. *J Stat Plan Inference*. 1999; 75: 305–318.

[2] Sun DC, Tsutakawa RK, He ZQ. Propriety of posteriors with improper priors in hierarchical linear mixed models. *Statistica Sinica*. 2001, 11: 77–95.

[3] Gilks WR, Richardson S, Spiegelhalter DJ. *Markov Chain Monte Carlo in Practice*. London, UK: Chapman & Hall; 1996.

[4] Gelman A, Rubin D. Inference from iterative simulation using multiple sequences. *Stat Sci*. 1992; 7:457–472.